Please amend the application as follows:

1. (original) A method for identifying phenotypes in cattle, the method comprising:

detecting a polymorphism present in the *IGF2* gene at position 150 of SEQ ID NO : 1 ; and

wherein the presence of a C residue (a C allele) is associated with phenotypes of at least one of increased rib eye area, decreased fat content and decreased marbling, as compared to cattle with a T residue (T allele) at position 150 of SEQ ID NO : 1.

2. (original) The method of Claim 1 wherein detecting the polymorphism comprises:

isolating a genomic DNA sample from cattle;

amplifying a region of the bovine *IGF2* gene using an oligonucleotide pair to form nucleic acid amplification products comprising amplified *IGF2* gene polymorphism sequences;

analyzing the amplification products to determine the presence or absence of at least one C allele.

3. (original) The method of Claim 2 wherein the oligonucleotide pair comprises SEQ ID NO: 2 and SEQ ID NO: 3.

4. (original) The method of Claim 3 wherein the polymorphism detected is a restriction fragment length polymorphism (RFLP).

5. (original) The method of Claim 4 wherein the RFLP is the presence or absence of a *BsrI* restriction site at nucleotide 150 in a nucleic acid amplification product produced by amplification of a portion of the *IGF2* gene using the oligonucleotide pair SEQ ID NO: 2 and SEQ ID NO : 3.

6. (original) The method of Claim 2 further comprising the inclusion of a detectable moiety such that the amplification product comprises a labeled amplification product.

7. (original) The method of Claim 6 wherein the detectable moiety is selected from the group consisting of fluorescent, bioluminescent, chemiluminescent, radioactive and colorigenic moieties.

8. (original) The method of Claim 1 further comprising:

contacting the nucleic acid amplification products with a hybridization probe;

wherein the hybridization probes comprise at least one oligonucleotide labeled with a detectable moiety;

under suitable conditions permitting hybridization of the at least one oligonucleotide to the amplification product to form a hybridization complex; and

wherein the presence of the detectable moiety in the hybridization complex indicates the presence of a *IGF2* polymorphism.

9. (original) The method of Claim 1 wherein the nucleic acid amplification product is produced by an amplification method selected from the group of polymerase chain reaction (PCR), strand displacement amplification (SDA), nucleic acid sequence based amplification (NASBA), rolling circle amplification, T7 polymerase mediated amplification, T3 polymerase mediated amplification and SP6 polymerase mediated amplification.

10. (original) An isolated and purified nucleic acid comprising a portion of the bovine *IGF2* gene, further comprising a polymorphism at position 150 as defined by the positions in SEQ ID NO: 1, and in which there is a C residue or a T residue at position 150.

11. (original) A method of selecting individual cattle based on the knowledge of an animal's *IGF2* genotype, comprising the steps of:

determining the *IGF2* alleles of an animal;

wherein the alleles of an animal are one of C/C, CT, or T/T with respect to position 150 of SEQ ID NO : 1; and

sorting animals into groups of like genotype; and

wherein a C/C or C/T genotype is associated with the phenotypes of increased rib-eye area, decreased fat content, and marbling as compared to T/T cattle.

12. (currently amended) A diagnostic kit for determining the ~~*IGF2*~~ genotype at position 150 of sequence ID NO: 1 in the *IGF2* gene of a bovine animal, the kit comprising:

oligonucleotide primers for amplifying a portion of the *IGF2* gene;

the primers comprising a forward primer comprising, at it's 3' end, sequence identical to at least 10 contiguous nucleotides within SEQ ID NO: 1;

a reverse primer comprising, at it's 3' end, a nucleotide sequence fully complementary to at least 10 contiguous nucleotides with SEQ ID NO: 1;

and wherein the forward and reverse primers will produce, in a PCR amplification reaction, a nucleic acid product amplification product containing a residue corresponding to position 150 of SEQ ID NO : 1.

13. (original) The kit of Claim 12 wherein the primers comprise the oligonucleotides SEQ ID NO: 2 and SEQ ID NO: 3.

14. (original) The kit of Claim 12 wherein the primers are labeled with a detectable moiety.

15. (original) The kit of Claim 12 further comprising at least one oligonucleotide, labeled with a detectable moiety and suitable for use as a hybridization probe.

16. (original) A method for identifying sires that will pass on a phenotype of lower birth weight to offspring, the method comprising:

detecting a polymorphism in a sire present in the *IGF2* gene at position 150 of SEQ ID NO : 1;

wherein the presence of a C residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (a C/C sire) is associated with the phenotype of production of offspring with lower birth weight, as compared to sires with a T residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (a T/T sire).

17. (original) The method of Claim 16 wherein detecting the polymorphism comprises:

isolating a genomic DNA sample from cattle;

amplifying a region of the bovine *IGF2* gene using an oligonucleotide pair to form nucleic acid amplification products comprising amplified *IGF2* gene polymorphism sequences;

analyzing the amplification products to determine the presence or absence of a C allele and a T allele.

18. (currently amended) A method of cattle production that reduces birth weight comprising breeding dams to sires having a C residue at position 150 of SEQ ID NO : 1 in both *IGF2* gene alleles (C/C sires).

19. (currently amended) A method of cattle production that increases birth weight comprising breeding dams to sires having a T residue at position 150 of SEQ ID NO: 1 in both *IGF2* gene alleles (T/T sires).